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TRANSMITTAL LETTER TO THE UNITED STATES

ATTORNEY'S DOCKET NUMBER 0817/00001

DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371

U.S. APPLICATION NO. (If known, see 37 CFR 1.5)

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/EP00/05862	23 June 2000	9 July 1999

TITLE OF INVENTION: IDENTIFICATION AND OVEREXPRESSION OF A DNA SEQUENCE ENCODING A
2-METHYL-6-PHYTYLHYDROQUINONE METHYLTRANSFERASE IN PLANTS

APPLICANT(S) FOR DO/EO/US Karin HERBERS, Ralf BADUR, Irene KUNZE, Michael GEIGER, Hans-Peter MOCK

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following
items and other information:

1. /X/ This is a FIRST submission of items concerning a filing under 35 U.S.C. 371.
 2. / / This is a SECOND or SUBSEQUENT submission of items concerning a filing under 35 U.S.C. 371.
 3. /X/ This express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and PCT Articles 22 and 39(1).
 4. /x / A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
 5. /X/ A copy of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. /X/ is transmitted herewith (required only if not transmitted by the International Bureau).
 - b. / / has been transmitted by the International Bureau.
 - c. / / is not required, as the application was filed in the United States Receiving Office (RO/USO).
 6. /X/ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
 7. / / Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3)).
 - a. / / are transmitted herewith (required only if not transmitted by the International Bureau).
 - b. / / have been transmitted by the International Bureau.
 - c. / / have not been made; however, the time limit for making such amendments has NOT expired.
 - d. / / have not been made and will not be made.
 8. / / A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
 9. / X / An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
 10. / / A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).
- Items 11. to 16. below concern other document(s) or information included:
11. / x / An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
 12. / X / An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
 13. / / A FIRST preliminary amendment.
/ / A SECOND or SUBSEQUENT preliminary amendment.
 14. / / A substitute specification.
 15. / / A change of power of attorney and/or address letter.
 16. /x / Other items or information.
International Search Report
International Preliminary Examination Report

U.S. Appln. No. (If Known) INTERNATIONAL APPLN. NO.
 PCT/EP00/05862


ATTORNEY'S DOCKET NO.
 0817/00001

	CALCULATIONS		PTO USE ONLY
17. /X/ The following fees are submitted			
BASIC NATIONAL FEE (37 CFR 1.492(a)(1)-(5)):			
Search Report has been prepared by the			
EPO or JPO.....\$890.00	890.00		
International preliminary examination fee paid to USPTO			
(37 CFR 1.482).....\$710.00			
No international preliminary examination fee paid to			
USPTO (37 CFR 1.482) but international search fee paid			
to USPTO (37 CFR 1.445(a)(2)).....\$740.00			
Neither international preliminary examination fee			
(37 CFR 1.482) nor international search fee			
(37 CFR 1.445(a)(2)) paid to USPTO\$ 1,040.00			
International preliminary examination fee paid to			
USPTO (37 CFR 1.482) and all claims satisfied pro			
-visions of PCT Article 33(2)-(4).....\$100.00			
ENTER APPROPRIATE BASIC FEE AMOUNT = \$ 890.00			
Surcharge of \$130.00 for furnishing the oath or declaration			
later than / / 20 / / 30 months from the earliest			
claimed priority date (37 CFR 1.492(e)).			
Claims	Number Filed	Number Extra	Rate
Total Claims	10	-20	X\$18.
Indep. Claims	5	-3	X\$84.
Multiple dependent claim(s) (if applicable)			+280.
TOTAL OF ABOVE CALCULATION		=	1,058.
Reduction of 1/2 for filing by small entity, if applicable.			
Verified Small Entity statement must also be filed			
(Note 37 CFR 1.9, 1.27, 1.28).			
SUBTOTAL		=	1,058.
Processing fee of \$130. for furnishing the English			
translation later than / / 20 / / 30 months from the			
earliest claimed priority date (37 CFR 1.492(f)).			
TOTAL NATIONAL FEE		=	1,058.
Fee for recording the enclosed assignment (37 CFR 1.21(h)).			
The assignment must be accompanied by an appropriate cover			
sheet (37 CFR 3.28, 3.31) \$40.00 per property			
TOTAL FEES ENCLOSED		=	\$ 1,098.00
		Amount to be	
		refunded:	\$
		Charged	\$

- a./X/ A check in the amount of \$ 1,098. to cover the above fees is enclosed.
- b./ / Please charge my Deposit Account No. _____ in the amount of \$ _____ to cover the above fees. A duplicate copy of this sheet is enclosed.
- c./X/ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 11-0345. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:
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 1101 Connecticut Ave., N.W.
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 SIGNATURE
 Herbert B. Keil
 NAME
 Registration No. 18,967

10019541.050602

PCT

IC20 Rec'd PCT/PTO 06 MAY 2002

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

10/019541

In re Application of

HERBERS et al.

Serial No. 10/019,541

Filed: January 3, 2002



Box PCT

For: IDENTIFICATION AND OVEREXPRESSION OF A DNA SEQUENCE
ENCODING A 2-METHYL-6-PHYTYLHYDROQUINONE
METHYLTRANSFERASE IN PLANTS

I hereby certify that this correspondence is being deposited with the
United States Postal Service as first class mail in an envelope
addressed to: Commissioner of Patents and Trademarks,
Washington, D.C. 20231, on:

Date of Deposit	May 3, 2002
Person Making Deposit	Herbert B. Keil
Signature	<i>Herbert B. Keil</i>
Date of Signature	May 3, 2002

Honorable Commissioner of
Patents and Trademarks
Washington, D.C. 20231

PRELIMINARY AMENDMENT
AND
RESPONSE TO NOTIFICATION OF MISSING REQUIREMENTS

Sir:

In response to the Notification of Missing Requirements under 35 USC § 371, a
copy of the Sequence Listing in computer readable form is attached hereto. The
content of the paper copy of the Sequence Listing and the copy of the Sequence Listing
in computer readable form is the same, and includes no new matter. Applicants also
attach replacement drawings which now have been translated completely English text.

HERBERS et al., Serial No. 10/019,541

AMENDMENTS

IN THE SPECIFICATION:

Delete the sequence listing in the specification pages 35-46 and substitute with the attached replacement sequence listing as separate pages 1-10.

Delete the drawings in the specification with the attached replacement drawings, which are now in English.

HERBERS et al., Serial No. 10/019,541

REMARKS

It is believed that by submitting the present amendment and sequence listing diskette, the application now fully complies with the requirements of 37 CFR 1.821-1.825. The enclosed drawings are simply English translations of the drawings filed with the application

Favorable action by the examiner is solicited.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

KEIL & WEINKAUF



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HBK/DSK/kas

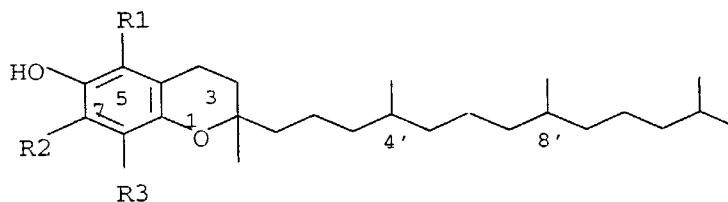
Identification and overexpression of a DNA sequence encoding a
2-methyl-6-phytylhydroquinone methyltransferase in plants

- 5 The invention relates to a DNA encoding a polypeptide with 2-methyl-6-phytylhydroquinone methyltransferase activity. Also, the invention relates to the use of DNA sequences encoding a polypeptide with 2-methyl-6-phytylhydroquinone methyltransferase activity for the generation of plants with an elevated tocopherol
10 and tocotrienol content, specifically to the use of the DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or DNA sequences hybridizing herewith or DNA sequences which are homologous to the full sequence or to subsequences, to a method for the generation of plants with an elevated tocopherol and tocotrienol content,
15 and to the resulting plant itself.

The generation of plants with an elevated sugar, enzyme and amino acid content has hitherto been an important objective in plant molecular genetics. The development of plants with an elevated
20 vitamin content, such as, for example, an elevated tocopherol and tocotrienol content, is, however, also of economic interest.

The naturally occurring eight compounds with vitamin E activity are derivatives of 6-chromanol (Ullmann's Encyclopedia of
25 Industrial Chemistry, Vol. A 27 (1996), VCH Verlagsgesellschaft, Chapter 4., 478-488, Vitamin E). The first group (1a-d) is derived from tocopherol, while the second group is composed of tocotrienol derivatives (2a-d):

30

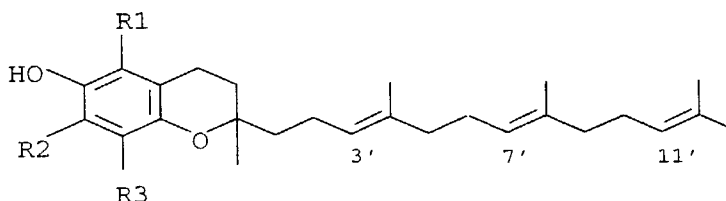


35

- 1a, α -tocopherol: $R^1 = R^2 = R^3 = \text{CH}_3$
1b, β -tocopherol [148-03-8]: $R^1 = R^3 = \text{CH}_3$, $R^2 = \text{H}$
1c, γ -tocopherol [54-28-4]: $R^1 = \text{H}$, $R^2 = R^3 = \text{CH}_3$
1d, δ -tocopherol [119-13-1]: $R^1 = R^2 = \text{H}$, $R^3 = \text{CH}_3$

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- 2a, α -tocotrienol [1721-51-3]: $R^1 = R^2 = R^3 = CH_3$
2b, β -tocotrienol [490-23-3]: $R^1 = R^3 = CH_3$, $R^2 = H$
2c, γ -tocotrienol [14101-61-2]: $R^1 = H$, $R^2 = R^3 = CH_3$
2d, δ -tocotrienol [25612-59-3]: $R^1 = R^2 = H$, $R^3 = CH_3$

5

α -Tocopherol has great economic importance.

The development of crop plants with an elevated tocopherol and tocotrienol content by means of conventional breeding is set a
10 limit.

The genetic engineering approach of isolating essential biosynthesis genes which encode, for example, tocopherol synthesis performance and introducing them into crop plants in a
15 directed fashion is a meaningful alternative. Knowledge of the biosynthesis and its regulation, and identification of genes which affect biosynthesis performance, are prerequisites for this method.

20 Isoprenoids or terpenoids are composed of a variety of classes of lipid-soluble molecules, and they are formed partially or exclusively from C_5 -isoprene units. Pure prenyl lipids (for example carotenoids) are composed of C skeletons based exclusively on isoprene units, while mixed prenyl lipids (for
25 example chlorophylls, tocopherols and vitamin K) have an isoprenoid side chain linked to an aromatic nucleus.

The biosynthesis of prenyl lipids starts with 3 x acetyl-CoA units which are converted into the starting isoprene unit (C_5),
30 namely isopentenyl pyrophosphate (IPP), via β -hydroxymethylglutaryl-CoA (HMG-CoA) and mevalonate. Recent *in vivo* C^{13} feeding experiments have demonstrated that the IPP formation pathway in various eubacteria, green algae and plant chloroplasts is mevalonate-independent. In this pathway,
35 hydroxyethylthiamine, which is formed by decarboxylation of pyruvate, and glyceraldehyde-3-phosphate (3-GAP) are first converted into 1-deoxy-D-xylulose-5-phosphate in a "transketolase" reaction mediated by 1-deoxy-D-xylulose-5-phosphate synthase (Lange et al., 1998;
40 Schwender et al., 1997; Arigoni et al., 1997; Lichtenthaler et al., 1997; Sprenger et al., 1997). In an intramolecular rearrangement reaction, this 1-deoxy-D-xylulose-5-phosphate is then converted into 2-C-methyl-D-erythritol-4-phosphate and then into IPP (Arigoni et al., 1997; Zeidler et al., 1998).
45 Biochemical data suggest that the mevalonate pathway operates in the cytosol and leads to the formation of phytosterols. The antibiotic mevinolin, a specific mevalonate formation inhibitor,

3

only leads to sterol biosynthesis inhibition in the cytoplasm, while prenyl lipid formation in the plastids remains unaffected (Bach and Lichtenthaler, 1993). In contrast, the mevalonate-independent pathway is located in the plastids and leads predominantly to the formation of carotenoids and plastid prenyl lipids (Schwender et al., 1997; Arigoni et al., 1997).

IPP is in equilibrium with its isomer, dimethylallyl pyrophosphate (DMAPP). Condensation of IPP with DMAPP head to tail results in the monoterpene (C₁₀) geranyl pyrophosphate (GPP). Addition of further IPP units results in the sesquiterpene (C₁₅) farnesyl pyrophosphate (FPP), and the diterpene (C₂₀) geranylgeranyl pyrophosphate (GGPP). Bonding between two GGPP molecules results in the formation of the C₄₀ precursors of carotenoids.

In the case of mixed prenyl lipids, the isoprene side chain, whose length varies, is linked to non-isoprene rings such as, for example, a porphyrine ring in the case of chlorophylls a and b. The chlorophylls and phylloquinones contain a C₂₀ phytyl chain, in which only the first isoprene unit contains a double bond. GGPP is converted by geranylgeranyl pyrophosphate oxidoreductase (GGPPOR) to give phytyl pyrophosphate (PPP), the starting material for the subsequent formation of tocopherols.

The ring structures of the mixed prenyl lipids which lead to the formation of vitamins E and K are quinones whose starting metabolites are derived from the shikimate pathway. The aromatic amino acids phenylalanine or tyrosine are converted into hydroxyphenyl pyruvate, which is dioxygenated to give homogentisic acid. Starting from erythrose-4-phosphate and phosphoenol pyruvate (PEP), the chorismate is formed by their condensation to give 3-deoxy-D-arabinoheptulosonate-7-phosphate (DAHP) via the intermediates of the shikimate pathway, 3'-dehydroquinate, 3'-dehydroshikimate, shikimate, shikimate-3-phosphate and 5'-enolpyruvylshikimate-3-phosphate. During this process, the erythrose-4-phosphate is formed in the Calvin cycle and the PEP is provided during glycolysis. The above-described homogentisic acid is subsequently bound to phytyl pyrophosphate (PPP) or geranylgeranyl pyrophosphate to form the precursors of α -tocopherol and α -tocotrienol, namely 2-methyl-6-phytylhydroquinone and 2-methyl-6-geranylgeranyl hydroquinone, respectively. Methylation steps with S-adenosylmethionine as methyl group donor lead first to 2,3-dimethyl-6-phytylquinol, subsequent cyclization leads to γ -tocopherol and further methylation to α -tocopherol (Richter,

5 directionally affect metabolite flow can be found in the literature. A direct effect on the quantities of carotenoids in these transgenic tomato plants was measured in experiments on an altered expression of phytoene synthase, which links two GGPP molecules to give 15-cis-phytoene (Fray and Grierson, Plant Mol. Biol. 22(4) (1993), 589-602; Fray et al., Plant J. 8 (1995), 693-701). As expected, transgenic tobacco plants which have reduced quantities of phenylalanine-ammonium lyase show reduced quantities of phenylpropanoid. The enzyme phenylalanine-ammonium lyase catalyzes the degradation of phenylalanine and thus
15 withdraws it from phenylpropanoid biosynthesis (Bate et al., Proc. Natl. Acad. Sci USA 91 (16) (1994): 7608-7612; Howles et al., Plant Physiol. 112 (1996), 1617-1624;).

30 It is an object of the present invention to develop a transgenic plant with an elevated tocopherol and tocotrienol content.

35 To this end, the activity of 2-methyl-6-phytylhydroquinone
methyltransferase (MPMT) was increased by overexpressing the
Synechocystis spec. PCC6803 MPMT gene in transgenic plants. This
may be achieved in principle by the expression of homologous or
40 heterologous MPMT genes.

Example 2 describes for the first time the cloning of an MPMT DNA sequence (SEQ ID No. 1) from *Synechocystis* spec. PCC6803. To ensure localization in the plastids, a transit signal sequence is arranged upstream of the *Synechocystis* MPMT nucleotide sequence (Fig. 3, Fig. 4). Another suitable expression cassette is a DNA sequence encoding an MPMT gene which hybridizes with SEQ ID No. 1

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or which is homologous to the full sequence or to subsequences and which is derived from other organisms or plants.

2,3-Dimethyl-6-phytylhydroquinone, of which larger quantities are now available owing to the additional expression of the MPMT gene, is reacted further toward tocopherols and tocotrienol (Figure 1).

The transgenic plants are generated by transforming the plants with a construct comprising the MPMT gene. Model plants employed for the production of tocopherols and tocotrienols were *Arabidopsis thaliana*, *Brassica napus* and *Nicotiana tabacum*.

Measurements on MPMT *Synechocystis* knock-out mutants showed a drastic decrease regarding the tocopherol and tocotrienol contents. This confirms the direct effect of plastid plant MPMT on tocopherol and tocotrienol synthesis.

The invention relates to the use of a *Synechocystis* spec. PCC6803 DNA sequence SEQ ID No. 1 which encodes an MPMT or its functional equivalents for the generation of a plant with an elevated tocopherol and tocotrienol content. The nucleic acid sequence may be, for example, a DNA or cDNA sequence. Encoding sequences which are suitable for insertion into an expression cassette are, for example, those which encode an MPMT and which allow the host to overproduce tocopherols and tocotrienols.

The expression cassettes also comprise regulatory nucleic acid sequences which govern the expression of the encoding sequence in the host cell. In a preferred embodiment, an expression cassette comprises a promoter upstream, i.e. on the 5'-end of the encoding sequence, and a polyadenylation signal downstream, i.e. on the 3'-end, and, if appropriate, further regulatory elements which are linked operatively with the sequence in between which encodes the MPMT gene. Operative linkage is to be understood as meaning the sequential arrangement of promoter, encoding sequence, terminator and, if appropriate, further regulatory elements in such a way that each of the regulatory elements can fulfill its function as intended when the encoding sequence is expressed. The sequences preferred for operative linkage, but not restricted thereto, are targeting sequences for guaranteeing subcellular localization in the apoplast, in the vacuole, in plastids, in the mitochondrion, in the endoplasmatic reticulum (ER), in the nucleus, in elaioplasts or in other compartments, and translation enhancers such as the tobacco mosaic virus 5'-leader sequence (Gallie et al., Nucl. Acids Res. 15 (1987), 8693-8711).

6

As an example, the plant expression cassette can be incorporated into a derivative of the transformation vector pBin-19 with 35S promoter (Bevan, M., Nucleic Acids Research 12 (1984): 8711-8721). Figure 4 shows a derivative of the transformation
5 vector pBin-19 with the seed-specific legumin B4 promoter.

A suitable promoter of the expression cassette is, in principle, any promoter which is capable of governing the expression of foreign genes in plants. In particular, a plant promoter or a
10 promoter derived from a plant virus is preferably used. Particularly preferred is the CaMV 35S promoter from cauliflower mosaic virus (Franck et al., Cell 21 (1980), 285 - 294). As is known, this promoter contains various recognition sequences for transcriptional effectors which in their totality lead to
15 permanent and constitutive expression of the introduced gene (Benfey et al., EMBO J. 8 (1989), 2195-2202).

The expression cassette may also comprise a chemically inducible promoter which allows expression of the exogenous MPMT gene in
20 the plant to be governed at a particular point in time. Examples of such promoters which can be used are, inter alia, the PRP1 promoter (Ward et al., Plant. Mol. Biol. 22 (1993), 361-366), a salicylic-acid-inducible promoter (WO 95/19443), a benzenesulfonamide-inducible promoter (EP-A 388186), a
25 tetracyclin-inducible promoter (Gatz et al., (1992) Plant J. 2, 397-404), an abscisic-acid-inducible promoter (EP-A 335528) or an ethanol- or cyclohexanone-inducible promoter (WO 93/21334).

Furthermore, particularly preferred promoters are those which
30 ensure expression in tissues or parts of the plant in which, for example, the biosynthesis of tocopherol or its precursors takes place. Promoters which ensure leaf-specific expression should be mentioned in particular. Promoters which should be mentioned are the potato cytosolic FBPase or the potato ST-LSI promoter
35 (Stockhaus et al., EMBO J. 8 (1989), 2445 - 245).

A foreign protein was expressed stably in the seeds of transgenic tobacco plants to an extent of 0.67% of the total soluble seed protein with the aid of a seed-specific promoter (Fiedler and
40 Conrad, Bio/Technology 10 (1995), 1090-1094). The expression cassette can therefore contain, for example, a seed-specific promoter (preferably the phaseolin promoter (US 5504200), the USP promoter (Baumlein, H. et al., Mol. Gen. Genet. (1991) 225 (3), 459 - 467) or the LEB4 promoter (Fiedler and Conrad, 1995)), the
45 LEB4 signal peptide, the gene to be expressed and an ER retention signal.

7

An expression cassette is generated by fusing a suitable promoter with a suitable MPMT DNA sequence and, preferably, a DNA which is inserted between promoter and MPMT DNA sequence and which encodes a chloroplast-specific transit peptide, and with a

5 polyadenylation signal, using customary recombination and cloning techniques as they are described, for example, by T. Maniatis, E.F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) and by T.J. Silhavy, M.L. Berman and L.W. Enquist,

10 Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and by Ausubel, F.M. et al., Current Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley-Interscience (1987).

15 Particularly preferred sequences are those which ensure targeting into the plastids.

Other expression cassettes which can be used are those whose DNA sequence encodes an MPMT fusion protein, part of the fusion

20 protein being a transit peptide which governs translocation of the polypeptide. Chloroplast-specific transit peptides which are cleaved off enzymatically from the MPMT residue after translocation of the MPMT gene into the chloroplasts are preferred. Particularly preferred is the transit peptide derived

25 from plastid *Nicotiana tabacum* transketolase or another transit peptide (for example the transit peptide of the Rubisco small subunit or of ferredoxin NADP oxidoreductase) or its functional equivalent.

30 Especially preferred are DNA sequences of three cassettes of the plastid transit peptide of tobacco plastid transketolase in three reading frames as KpnI/BamHI fragments with an ATG codon in the NcoI cleavage site:

35 pTP09

KpnI_GGTACCATGGCGTCTTCTTCTTCTCTCACTCTCTCTCAAGCTATCCTCTCTCGTTCTGTC
CCTCGCCATGGCTCTGCCTCTTCTTCTCAACTTTCCCTTCTTCTCTCACTTTTCCGGCCTTAA
ATCCAATCCCAATATCACCACTCCCGCCGCGTACTCCTTCTCTCGCCGCCGCCGCCGCGCTCG
40 TAAGGTCACCGCGATTTCGTGCCTCAGCTGCAACCGAAACCATAGAGAAAAGTACTGCGGGA
TCC_BamHI

pTP10

45 KpnI_GGTACCATGGCGTCTTCTTCTTCTCTCACTCTCTCTCAAGCTATCCTCTCTCGTTCTGTC
CCTCGCCATGGCTCTGCCTCTTCTTCTCAACTTTCCCTTCTTCTCTCACTTTTCCGGCCTTAA
ATCCAATCCCAATATCACCACTCCCGCCGCGTACTCCTTCTCTCGCCGCCGCCGCCGCGCTCG

8

TAAGGTCACCGGCGATTTCGTGCCTCAGCTGCAACCGAAACCATAGAGAAAAGTGAAGTGCCTG
GATCC_BamHI

pTP11

5

KpnI_GGTACCATGGCGTCTTCTTCTCTCACTCTCTCAAGCTATCCTCTCTCGTTCTGTC
CCTCGCCATGGCTCTGCCTCTTCTTCTCAACTTTCCCCTTCTTCTCTCACTTTTCCGGCCTTAA
ATCCAATCCCAATATCACCACCTCCCGCCGCGTACTCCTTCTCCGCGCCGCGCGCGCGCTCG
TAAGGTCACCGGCGATTTCGTGCCTCAGCTGCAACCGAAACCATAGAGAAAAGTGAAGTGCCTG

10 ATCC_BamHI

The inserted nucleotide sequence encoding an MPMT can be prepared synthetically, obtained naturally or contain a mixture of synthetic and natural DNA constituents, and may be composed of various heterologous MPMT gene segments of a variety of organisms. In general, synthetic nucleotide sequences are produced which are equipped with codons which are preferred by plants. These codons which are preferred by plants can be determined from codons with the highest protein frequency expressed in the majority of interesting plant species. When preparing an expression cassette, a variety of DNA fragments may be manipulated in order to obtain a nucleotide sequence which expediently reads in the correct direction and which is equipped with a correct reading frame. Adaptors or linkers may be added to the fragments in order to link the DNA fragments to each other.

The promoter and terminator regions may expediently be provided, in the direction of transcription, with a linker or polylinker containing one or more restriction sites for insertion of this sequence. As a rule, the linker has 1 to 10, in most cases 1 to 8, preferably 2 to 6, restriction sites. In general, the linker within the regulatory regions has a size less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be native, or homologous, or else foreign, or heterologous, to the host plant. The expression cassette comprises, in the 5'-3' direction of transcription, the promoter, a DNA sequence encoding an MPMT gene, and a region for transcriptional termination. Various termination regions may be exchanged for each other as desired.

40

Manipulations which provide suitable restriction cleavage sites or which eliminate the excess DNA or restriction cleavage sites may also be employed. *In vitro* mutagenesis, primer repair, restriction or ligation may be used in cases where insertions, deletions or substitutions such as, for example, transitions and transversions are suitable. Complementary ends of the fragments may be provided for ligation in the case of suitable

manipulations such as, for example, restriction, chewing back or filling in overhangs for blunt ends.

Preferred polyadenylation signals are plant polyadenylation signals, preferably those which correspond essentially to *Agrobacterium tumefaciens* T-DNA-polyadenylation signals, in particular those of gene 3 of the T-DNA (octopine synthase) of the Ti-plasmid pTiACH5 (Gielen et al., EMBO J. 3 (1984), 835 et seq.), or functional equivalents.

10

The fused expression cassette which encodes an MPMT gene is preferably cloned into a vector, for example pBin19, which is suitable for transforming *Agrobacterium tumefaciens*. *Agrobacteria* transformed with such a vector can then be used in a known manner for transforming plants, in particular crop plants, such as, for example, tobacco plants, for example by bathing wounded leaves or leaf sections in an *agrobacterial* suspension and subsequently growing them in suitable media. The transformation of plants by *agrobacteria* is known, inter alia, from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, edited by S.D. Kung and R. Wu, Academic Press, 1993, pp. 15 - 38. Transgenic plants which comprise, integrated into the expression cassette, a gene for expressing an MPMT gene can be regenerated in a known manner from the transformed cells of the wounded leaves or leaf sections.

To transform a host plant with a DNA encoding an MPMT, an expression cassette is inserted into a recombinant vector whose vector DNA comprises additional functional regulatory signals, for example sequences for replication or integration. Suitable vectors are described, inter alia, in "Methods in Plant Molecular Biology and Biotechnology" (CRC Press), chapter 6/7, (1993), pp. 71 - 119.

Using the above-cited recombination and cloning techniques, the expression cassettes can be cloned into suitable vectors which allow their multiplication, for example in *E. coli*. Suitable cloning vectors are, inter alia, pBR332, pUC series, M13mp series and pACYC184. Especially suitable are binary vectors which are capable of replication in *E. coli* and in *agrobacteria*.

The invention furthermore relates to the use of an expression cassette comprising a DNA sequence SEQ ID No. 1 or a DNA sequence hybridizing herewith for transforming plants, plant cells, plant tissues or parts of plants. The preferred object of the use is an elevated tocopherol and tocotrienol content of the plant.

10

Depending on the choice of promoter, expression may take place specifically in the leaves, in the seeds, the petals or in other parts of the plant. Such transgenic plants, their propagation material and the cells, tissues or parts of such plants are a
5 further subject of the present invention.

In addition, the expression cassette may also be employed for transforming bacteria, cyanobacteria, yeasts, filamentous fungi and algae for the purpose of increasing the tocopherol and
10 tocotrienol content.

The transfer of foreign genes into the genome of a plant is termed transformation. It exploits the above-described methods of transforming and regenerating plants from plant tissues or plant
15 cells for transient or stable transformation. Suitable methods are protoplast transformation by polyethylene-glycol-induced DNA uptake, the biolistic method using the gene gun - the so-called particle bombardment method, electroporation, incubation of dry embryos in DNA-containing solution, microinjection and
20 agrobacterium-mediated gene transfer. The abovementioned methods are described, for example, in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, edited by S.D. Kung and R. Wu, Academic Press (1993), 128 - 143, and in Potrykus, Annu. Rev. Plant Physiol.
25 Plant Molec. Biol. 42 (1991), 205 - 225. The construct to be expressed is preferably cloned into a vector which is suitable for the transformation of Agrobacterium tumefaciens, for example pBin19 (Bevan et al., Nucl. Acids Res. 12 (1984), 8711).

30 Agrobacteria transformed with an expression cassette can equally be used in a known manner for transforming plants, in particular crop plants such as cereals, corn, oats, soya, rice, cotton, sugar beet, canola, sunflower, flax, hemp, potato, tobacco, tomato, oilseed rape, alfalfa, lettuce and the various tree, nut
35 and grapevine species, for example by bathing wounded leaves or leaf sections in an agrobacterial suspension and subsequently growing them in suitable media.

Functionally equivalent sequences which encode an MPMT gene are
40 those sequences which still have the desired functions, despite a differing nucleotide sequence. Functional equivalents thus encompass naturally occurring variants of the sequences described herein, and synthetic nucleotide sequences, for example those obtained by chemical synthesis and adapted to suit the codon
45 usage of a plant.

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Functional equivalents are also to be understood as meaning, in particular, natural or artificial mutations of an originally isolated sequence encoding an MPMT which continue to show the desired function. Mutations encompass substitutions, additions, 5 deletions, exchanges or insertions of one or more nucleotide residues. Thus, the present invention also encompasses, for example, those nucleotide sequences which are obtained by modifying the MPMT nucleotide sequence. The purpose of such a modification may be, for example, the further limitation of the 10 encoding sequence contained therein or else, for example, the insertion of further restriction enzyme cleavage sites.

Example 8 describes a deletion clone of the MPMT gene, see SEQ ID No. 7.

15

Functional equivalents are also those variants whose function is attenuated or increased compared with the starting gene, or gene fragment.

20 Also suitable are artificial DNA sequences as long as they mediate the desired characteristic, for example an elevated tocopherol content in the plant, by overexpression of an MPMT gene in crop plants, as described above. Such artificial DNA sequences can be identified, for example, by backtranslation of 25 proteins with MPMT activity which have been constructed by means of molecular modeling, or else by *in vitro* selection. Especially suitable are encoding DNA sequences which have been obtained by backtranslating a polypeptide sequence in accordance with the host-plant-specific codon usage. An expert skilled in the art of 30 plant genetic engineering methods will readily be able to identify the specific codon usage by computer evaluations of other known genes of the plant to be transformed.

Further suitable equivalent nucleic acid sequences which should 35 be mentioned are sequences which encode fusion proteins, an MPMT polypeptide or a functionally equivalent portion thereof being a constituent of the fusion protein. The second part of the fusion protein may be, for example, another enzymatically active polypeptide, or an antigenic polypeptide sequence with the aid of 40 which detection of MPMT expression is possible (for example myc-tag or his-tag). However, it is preferably a regulatory protein sequence such as, for example, a transit peptide which leads the MPMT protein to the plastids.

45 An elevated tocopherol and tocotrienol content is to be understood as meaning for the purposes of the present invention the artificially acquired ability to increase biosynthetic

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performance regarding these compounds by functional overexpression of an MPMT gene SEQ ID No. 1 or SEQ ID No. 7 in the plant in comparison with the non-genetically modified plant for at least one plant generation.

5

Both the tocopherol content and the tocotrienol content can be increased. It is preferred to increase the tocopherol content. However, under certain conditions, it is also possible preferentially to increase the tocotrienol content.

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The tocopherol biosynthesis site, for example, is inter alia the leaf tissue, so that leaf-specific expression of the MPMT gene is meaningful. However, it is obvious that tocopherol biosynthesis need not be limited to the leaf tissue but may also take place in

15 a tissue-specific fashion in all of the other remaining parts of the plant, for example in fatty seeds.

The constitutive expression of the exogenous MPMT gene is also advantageous. On the other hand, inducible expression may also be
20 desirable.

The expression efficacy of the transgenically expressed MPMT gene can be determined, for example, *in vitro* by shoot meristem propagation. In addition, altered expression of the MPMT gene
25 with regard to type and level, and its effect on tocopherol biosynthesis performance may be tested on test plants in greenhouse experiments.

The invention furthermore relates to transgenic plants,
30 transformed with an expression cassette comprising the sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith or a DNA sequence which is homologous to the full sequence or to subsequences, and to transgenic cells, tissues, parts and propagation material of such plants. Especially
35 preferred are transgenic crop plants such as, for example, barley, wheat, rye, corn, oats, soya, rice, cotton, sugar beet, canola, sunflower, flax, hemp, potato, tobacco, tomato, oilseed rape, alfalfa, tagetes, lettuce and the various tree, nut and grapevine species.

40

Plants for the purposes of the invention are mono- and dicotyledonous plants.

The invention furthermore relates to photosynthetically active
45 organisms transformed with an expression cassette containing the sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith or a DNA sequence which is homologous to the

full sequence or to subsequences. Examples of photosynthetically active organisms are, besides the plants, cyanobacteria, mosses and algae.

As already mentioned, MPMT is a potential target for herbicides. To find efficient MPMT inhibitors, it is necessary to provide suitable test systems with which inhibitor-enzyme binding studies can be carried out. To this end, for example, the complete cDNA sequence of the Synechocystis MPMT is cloned into an expression vector (pQE, Qiagen) and overexpressed in *E. coli*.

The MPMT protein which is expressed with the aid of the expression cassette according to the invention is particularly suitable for finding MPMT-specific inhibitors.

30 The test system according to the invention allows a large number of chemical compounds to be checked rapidly and simply for herbicidal properties. The method allows reproducibly and specifically to select, from a large number of substances, those

35 with high potency in order subsequently to carry out, with these substances, further, in-depth tests with which the skilled worker is familiar.

Overexpression of the MPMT-encoding gene sequence SEQ ID No. 1 or SEQ ID No. 7 in a plant allows an improved resistance to MPMT inhibitors to be achieved. Transgenic plants generated thus are also a subject of the invention.

14

The MPMT protein prepared using the DNA sequence SEQ ID No. 1 or SEQ ID No. 7 is also suitable for carrying out biotransformations for providing substantial amounts of 2,3-dimethyl-6-phytylhydroquinone. To do this,

5 2-methyl-6-phytylhydroquinone is converted in the presence of the enzyme MPMT and the co-substrate S-adenosyl-L-methionine to give 2,3-dimethyl-6-phytylhydroquinone. In principle, the biotransformation can be carried out on entire cells which express the enzyme MPMT, or on cell extracts of these cells, or

10 else on purified or ultrapure MPMT in the presence of S-adenosyl-L-methionine.

The invention furthermore relates to:

- 15 - Methods for the transformation of a plant, which comprise introducing, into a plant cell or protoplasts of plants, expression cassettes containing a DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith or a
- 20 DNA sequence which is homologous to the full sequence or to subsequences, and regenerating these to give entire plants.
- The use of the DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith for the generation of plants with an elevated tocopherol and tocotrienol content by
- 25 expressing, in plants, an MPMT DNA sequence.

The invention is illustrated by the examples which follow, but not limited thereto.

30 Sequence analysis of recombinant DNA

Recombinant DNA molecules were sequenced using a laser fluorescence DNA sequencer by Licor (sold by MWG Biotech, Ebersbach) using the method of Sanger (Sanger et al., Proc. Natl.

35 Acad. Sci. USA 74 (1977), 5463 - 5467).

Example 1

Identification of a *Synechocystis* spec. PCC6803

40 2-methyl-6-phytylhydroquinone methyltransferase

The *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase was cloned and identified as follows:

- 45 Using a sequence motif conserved in S-adenosyl-L-methionine methyltransferases which is responsible for binding S-adenosyl-L-methionine (SAM) (C.P. Joshi and V.L. Chiang. PMB.

15

- 37 (1998): 663-374), a *Synechocystis* spec. PCC6803 genomic DNA database was screened (Kaneko et al., DNA Res. 34 (1996): 109-136). The hypothetical proteins identified during this screening which contained the SAM binding motif were compared
- 5 with the primary sequences of the *Synechocystis* spec. PCC6803 γ -tocopherol methyltransferase (termed slr0089) and the *Arabidopsis thaliana* γ -tocopherol methyltransferase (David Shintani and Dean DellaPenna. Science. 282 (1998): 2098-2100).
- 10 It was possible to identify a hypothetical protein (termed sl10418 SEQ.-ID No. 2) whose amino acid sequence corresponded to a low degree with the γ -tocopherol methyl transferases from *Synechocystis* spec. PCC6803 and *Arabidopsis thaliana* (36% and 28% identity, respectively).
- 15 Further studies of the primary sequence of the hypothetical protein sl10418 confirmed the existence of a putative prokaryotic signal sequence within the first 20 amino acids (PSIGNAL, PC/GENE™ IntelliGenetics, Inc (1991). Such a sequence was also
- 20 identified in *Synechocystis* spec. PCC6803 γ -tocopherol methyltransferase (slr0089) (D. Shintani and D. DellaPenna. Science. 282 (1998): 2098-2100) and suggests the identical localization of the two proteins.
- 25 The predicted molecular weight of the unprocessed protein is 34.9 kDa and is thus within a range which had also been determined for the *Synechocystis* spec. PCC6803 γ -tocopherol methyltransferase (David Shintani and Dean DellaPenna, Science. 282 (1998): 2098-2100) and for the γ -tocopherol methyltransferase
- 30 purified from bell peppers (d'Harlingue and Camara, Plastid enzymes of terpenoid biosynthesis: Purification of γ -Tocopherol Methyltransferase from *Capsicum* Chromoplasts. Journal of Biological Chemistry, Vol. 269 (1985), No.28, 15200-15203).
- 35 Taking into consideration the facts, we concluded that the hypothetical protein sl10418 might be a tocopherol methyltransferase.

Example 2

- 40 Amplification and cloning of the *Synechocystis* spec. PCC 6803 2-methyl-6-phytylhydroquinone methyltransferase
- The DNA encoding the ORF (open reading frame) sl10418 was
- 45 amplified by means of polymerase chain reaction (PCR) from *Synechocystis* spec. PCC6803 following the method of Crispin A. Howitt (BioTechniques 21, July 1996:32-34) using a sense-specific

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primer (sll04185' SEQ ID No. 5) and an antisense-specific primer (sll04183' SEQ ID No. 6).

The PCR conditions were as follows:

5

The PCR was carried out in a 50 µl reaction batch which contained:

- 5 µl of a *Synechocystis* spec. PCC6803 cell suspension
- 10 - 0.2 mM dATP, dTTP, dGTP, dCTP
- 1.5 mM Mg(OAc)₂
- 5 µg bovine serum albumin
- 40 pmol sll04185'
- 40 pmol sll04183'
- 15 - 15 µl 3.3 × rTth DNA polymerase XL buffer (PE Applied Biosystems)
- 5U rTth DNA polymerase XL (PE Applied Biosystems)

The PCR was carried out under the following cycle conditions:

20

Step 1: 5 minutes at 94°C (denaturing)

Step 2: 3 seconds at 94°C

Step 3: 2 minutes at 58°C (annealing)

Step 4: 2 minutes at 72°C (elongation)

25 40 repetitions of steps 2-4

Step 5: 10 minutes at 72°C (post-elongation)

Step 6: 4°C (waiting loop)

The amplicon was cloned into the PCR cloning vector pGEM-T

30 (Promega) using standard methods. The identity of the amplicon generated was confirmed by sequencing using the M13F (-40) primer.

Example 3

35

Generation of an sll0418 knock-out mutant

A DNA construct to generate a deletion mutant of the ORF sll0418 in *Synechocystis* spec. PCC6803 was generated using standard

40 cloning techniques.

The vector pGEM-T/sll0418 was digested using the restriction enzyme *Bal*I. The presence of two *Bal*I cleavage sites within the sll0418 sequence (position bp 109 and bp 202, respectively)

45 resulted in the loss of a 93-bp internal fragment. The aminoglycoside-3'-phosphotransferase of the transposon Tn903 was cloned into the *Bal*I cleavage sites of the sll0418 ORF. To this

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end, the Tn903 was isolated as an EcoRI fragment from the vector pUC4k (Vieira, J and Messing, J, Gene: 19 (1982), 259-268), the overhangs of the restriction digest were made blunt-ended by standard methods and ligated into the BalI-cut vector

5 pGEM-T/sll0418. The ligation batch was used for the transformation of *E. coli* Xl1 blue cells. Transformants were selected by using kanamycin and ampicillin. A recombinant plasmid (pGEM-T/sll0418::tn903) was isolated and employed in the transformation of *Synechocystis spec.* PCC6803 following the

10 method of Williams (Methods Enzymol. 167 (1987), 776-778).

Synechocystis spec. PCC6803 transformants were selected on kanamycin-containing (kan) solid BG-11 medium (Castenholz, Methods in Enzymology (1988), 68-93) at 28°C and 30 $\mu\text{mol photons}$

15 $\times (\text{m}^2 \times \text{s})^{-1}$. After five selection cycles (passages of single colonies onto fresh BG-11 kan medium), four independent knock-out mutants were generated.

The complete loss of the sll0418 endogene or the exchange for the

20 recombinant sll0418::tn903 DNA was confirmed by PCR analyses.

Example 4

Comparison of the tocopherol production in *Synechocystis spec.*

25 PCC6803 wild-type cells and the generated knock-out mutants of ORF sll0418

The cells of the four independent *Synechocystis spec.* PCC68033 knock-out mutants of ORF sll0418 which were cultured on the BG-11

30 kan agar medium and untransformed wild-type cells were used to inoculate liquid cultures. These cultures were grown for approximately 3 days at 28°C and 30 $\mu\text{mol photons} \times (\text{m}^2 \times \text{s})^{-1}$ (30 μE). After determining the OD₇₃₀ of the individual cultures, the OD₇₃₀ of all cultures was synchronized by suitable dilutions

35 with BG-11 (wild types) or BG-11 kan (mutants). These cell-density-synchronized cultures were used to inoculate three cultures per mutant and the wild-type controls. Thus, the biochemical analyses were carried out using in each case three independently grown cultures of a mutant and the corresponding

40 wild types. The cultures were grown to an optical density of OD₇₃₀=0.3. The cell culture medium was removed by two centrifugation steps at 14,000 rpm in an Eppendorf bench centrifuge. The cells were subsequently disrupted by four incubations for 15 minutes in an Eppendorf shaker at 30°C,

45 1000 rpm, in 100% methanol, and the supernatants obtained in each

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case were combined. Further incubation steps resulted in no further release of tocopherols or tocotrienols.

To avoid oxidation, the resulting extracts were analyzed directly
5 after extraction with the aid of a Waters Allience 2690 HPLC system. Tocopherols and tocotrienols were separated over a reverse phase column (ProntoSil 200-3-C30, Bischoff) using a mobile phase of 100% methanol, and identified with reference to standards (Merck). The detection system used was the fluorescence
10 of the substances (excitation 295 nm, emission 320 nm), which was detected with the aid of a Jasco fluorescence detector FP 920.

In the *Synechocystis* spec. PCC6803 knock-out mutants of ORF sll0418, no tocopherols or tocotrienols were found. However,
15 tocopherols and tocotrienols were measured in the *Synechocystis* spec. PCC6803 wild-type cells.

The loss of the ability to produce tocopherols and tocotrienols within the knock-out mutants of ORF sll0418 in comparison with
20 the *Synechocystis* spec. PCC6803 wild-type cells demonstrates that the gene sll0418 encodes a 2-methyl-6-phytylhydroquinone methyltransferase.

Example 5

25

Functional characterization of the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase by heterologous expression in *E. coli*

30 The hypothetical *Synechocystis* spec. PCC6803 protein sll0418 was identified by functional expression in *E. coli* as 2-methyl-6-phytylhydroquinone methyltransferase.

The gene sll0418 which had been amplified from *Synechocystis*
35 spec. PCC6803 was subcloned into the expression vector pQE-30 (Qiagen) in the correct reading frame. The primers sll04185' and sll04183' (SEQ ID No. 5 and 6, respectively) which had been used for amplifying the ORF sll0418 from *Synechocystis* spec. PCC6803, were constructed in such a way that BamHI restriction cleavage
40 sites were added to the 5' end and the 3' end of the amplicon; see SEQ ID No. 3. Using these flanking BamHI restriction cleavage sites, the sll0418 fragment was isolated from the recombinant plasmid pGEM-T/sll0418 and ligated into a BamHI-cut pQE-30 using standard methods. The ligation batch was used for the
45 transformation of M15 *E. coli* cells, and kanamycin- and ampicillin-resistant transformants were analyzed. The kanamycin resistance is mediated by the pREP-4 plasmid, which is contained

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in the M15 cells. A recombinant plasmid (pQE-30/sll0418) which carried the sll0418 fragment in the correct orientation was isolated. Identity and orientation of the insert were confirmed by sequencing.

- 5 The recombinant plasmid pQE-30/sll0418 was used for the transformation of M15 *E. coli* cells in order to generate recombinant sll0418 protein. Using a colony which originated from the transformation, an overnight culture in Luria broth medium
- 10 supplemented with 200 µg/ml ampicillin (Amp) and 50 µg/ml kanamycin (Kan) was inoculated. Starting from this culture, a 100 ml Luria broth culture (Amp/Kan) was inoculated the morning thereafter. This culture was incubated at 28°C on a shaker incubator until an OD₆₀₀ of 0.35-0.4 was reached. Then, production
- 15 of the recombinant protein was induced by adding 0.4 mM isopropyl-β-D-thiogalactopyranoside (IPTG). The culture was shaken for a further 3 hours at 28°C and the cells were subsequently pelleted by centrifugation at 8000 g.
- 20 The pellet was resuspended in 600 µl lysis buffer (approx. 1-1.5 ml/g pellet moist weight, 10 mM HEPES KOH pH 7.8, 5 mM dithiothreitol (DTT), 0.24 M sorbitol). Then, PMSF (phenyl methylsulfonate) was added to a final concentration of 0.15 mM and the batch was placed on ice for 10 minutes. The cells were
- 25 disrupted by a 10-second ultrasonic pulse using an ultrasonic processor. After addition of Triton X100 (final concentration 0.1%), the cell suspension was incubated on ice for 30 minutes. The batch was subsequently centrifuged for 30 minutes at 25,000 x g and the supernatant was employed in the assay.
- 30 The 2-methyl-6-phytylhydroquinone methyltransferase activity was determined by detecting the radiolabeled reaction product 2,3-dimethyl-6-phytylhydroquinone.
- 35 To this end, 135 µl of the enzyme (approx. 300-600 µg) together with 20 µl of substrate (2-methyl-6-phytylhydroquinone) and 15 µl (0.46 mM SAM ¹⁴C) methyl group donor were incubated for 4 hours in the dark at 25°C in the following reaction buffer: 200 µl (125 mM) tricine-NaOH pH 7.6, 100 µl (1.25 mM) sorbitol, 10 µl (50 mM)
- 40 MgCl₂ and 20 µl (250 mM) ascorbate.

- The reaction was quenched by adding 750 µl of chloroform/methanol (1:2) + 150 µl of 0.9% NaCl. The mixed batch was centrifuged briefly, and the top phase was discarded. The bottom phase is
- 45 transferred into a new reaction vessel and evaporated under nitrogen. The residues were taken up in 20 µl of ether and applied to a thin-layer plate in order to separate the substances

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by chromatography (solid phase: HPTLC plates: silica gel 60 F₂₅₄ (Merck), liquid phase: toluene). The radiolabeled reaction product is detected by using a phosphoimager.

- 5 These experiments confirm that the protein encoded by the *Synechocystis* spec. PCC6803 gene sl10418 (SEQ ID No.1) is a 2-methyl-6-phytylhydroquinone methyltransferase since it has the enzymatic activity to convert 2-methyl-6-phytylhydroquinone into 2,3-dimethyl-6-phytylhydroquinone.

10

Figure 2 shows a sequence comparison at amino acid level between the γ -tocopherol methyltransferases from *Synechocystis* spec. PCC *Synechocystis* spec. PCC6803 (slr0089) and *A.thaliana* (aratmt) with the 2-methyl-6-phytylhydroquinone methyltransferase

- 15 (sl104189) from *Synechocystis* spec. PCC6803. The correspondence with the γ -tocopherol methyltransferases from *Synechocystis* spec. PCC6803 and *Arabisopsis thaliana* is 36 and 28% identity, respectively.

20 Example 6

Substrate specificity of the 2-methyl-6-phytylhydroquinone methyltransferase

- 25 Enzymatic studies as carried out in Example 5 confirm that the enzyme MPMT - encoded by the *Synechocystis* spec. PCC6803 gene sl10418 (SEQ-ID No. 1) - converts 2-methyl-6-phytylhydroquinone in 2,3-dimethyl-6-phytylhydroquinone.

- 30 In addition, the enzyme MPMT has a 2-methyl-6-geranyl-geranylhydroquinone methyltransferase activity, while a γ -tocopherol methyltransferase activity could not be detected. This confirms that the enzyme 2-methyl-6-phytylhydroquinone methyltransferase participates in tocotrienol biosynthesis since
- 35 it converts 2-methyl-6-geranylgeranylhydroquinone into 2,3-dimethyl-6-geranylgeranylhydroquinone. This clearly demonstrates that the enzyme activity of the 2-methyl-6-phytylhydroquinone methyltransferase differs from that of γ -tocopherol methyltransferase.

40

Example 7

Generation of expression cassettes containing the MPMT gene

- 45 Transgenic plants were generated which express the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase firstly under the control of the constitutive CaMV (cauliflower

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mosaic virus) 35S promoter (Franck et al., cell 21 (1980), 285-294) and secondly under the control of the seed-specific promoter of the *Vicia faba* legumin gene (Kafatos et al., Nuc. Acid. Res., 14(6) (1986), 2707-2720). The basis of the plasmid

5 generated for the constitutive expression of the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase was pBinAR-TkTp-9 (Ralf Badur, PhD thesis, University of Göttingen, 1998). This vector is a derivative of pBinAR (Höfgen and Willmitzer, Plant Sci. 66 (1990), 221-230) and contains the CaMV

10 (cauliflower mosaic virus) 35S promoter (Franck et al., 1980), the termination signal of the octopine synthase gene (Gielen et al., EMBO J. 3 (1984), 835-846) and the DNA sequence encoding the transit peptide of the *Nicotiana tabacum* plastid transketolase (Ralf Badur, PhD thesis, University of Göttingen, 1998). Cloning

15 the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase into this vector taking into consideration the correct reading frame generates a translational fusion of the 2-methyl-6-phytylhydroquinone methyltransferase with the plastid transit peptide. The transgene is thus transported to the

20 plastids.

To generate this plasmid, the gene sll0418 was isolated from plasmid pGEM-T/sll0418 using the flanking BamHI restriction cleavage sites. This fragment was ligated into a BamHI-cut

25 pBinAR-TkTp-9 using standard methods (see Figure 3). This plasmid (pBinAR-TkTp-9/sll0418) was used for the generation of transgenic *Arabidopsis thaliana*, *Brassica napus* and *Nicotiana tabacum* plants. Fragment A (529 bp) in Figure 3 contains the CaMV 35S promoter (nucleotides 6909 to 7437 of cauliflower mosaic virus),

30 fragment B (245 bp) encodes the transit peptide of the *Nicotiana tabacum* transketolase, fragment C (977 bp) encodes the *Synechocystis* spec. PCC6803 ORF sll0418, and fragment D (219 bp) encodes the termination signal of the octopine synthase gene.

35 To generate a plasmid which allows the seed-specific expression of the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase in plants, the seed-specific promoter of the legumin B4 gene (Kafatos et al., Nuc. Acid. Res., 14(6) (1986), 2707-2720), was used. The 2.7 kb fragment of the legumin B4 gene

40 promoter was isolated from plasmid pCR-Script/lePOCS using the EcoRI cleavage site and the KpnI cleavage site which flank the promoter at the 5' and at the 3' end, respectively. Plasmid pBinAR-TkTp-9/sll0418 was also treated with the restriction enzymes EcoRI and KpnI. As a consequence, the CaMV 35S promoter

45 was excised from this plasmid. The promoter of the legumin gene was subsequently cloned into this vector as EcoRI/KpnI fragment, thus generating a plasmid which placed the expression of gene

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sll0418 under the control of this seed-specific promoter, see Figure 4. This plasmid (pBinARleP-TkTp-9/sll0418) was used for the generation of transgenic *Arabidopsis thaliana*, *Brassica napus* and *Nicotiana tabacum* plants.

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Fragment A (2700 bp) in Figure 4 contains the promoter of the *Vicia faba* legumin B4 gene, fragment B (245 bp) encodes the transit peptide of the *Nicotiana tabacum* transketolase, fragment C (977 bp) encodes the *Synechocystis* spec. PCC6803 ORF sll0418, and fragment D (219 bp) encodes the termination signal of the octopine synthase gene.

10

Example 8

- 15 Generation of expression cassettes containing a deletion clone of the MPMT gene

Based on a computer analysis, a putative prokaryotic secretion signal was identified in the primary sequence of ORF sll0418. To ensure that this has no adverse effect on the import of the protein into the plastids upon expression in plants, a derivative of the sequence of sll0418 was generated in which the putative secretion signal was deleted (SEQ ID No. 7). This deletion was carried out using PCR technology. By virtue of the primers used for this purpose (sll0418DSp5', SEQ ID No. 9 and sll0418DSp3', SEQ ID No. 10), an EcoRV restriction cleavage site was added onto the 5' end of the sequence and an SalI restriction cleavage site onto the 3' end, thus allowing directed cloning into vector pBinAR-TkTp-9. The resulting plasmid pBinAR-TkTp-9/sll0418 Δ SP is described in Figure 5. Fragment A (529 bp) in Figure 5 contains the CaMV 35S promoter (nucleotides 6909 to 7437 of the cauliflower mosaic virus), fragment B (245 bp) encodes the transit peptide of the *Nicotiana tabacum* transketolase, fragment C (930 bp) encodes the *Synechocystis* spec. PCC6803 ORF sll0418 Δ SP, and fragment D (219 bp) encodes the termination signal of the octopine synthase gene.

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To generate a plasmid which allows the seed-specific expression of the deletion clone of the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase in plants, the seed-specific promoter of the legumin B4 gene which has already been described was used again (Kafatos et al., Nuc. Acid. Res., 14(6) (1986), 2707-2720). The 2.7 kb fragment of the legumin B4 gene promoter was isolated from plasmid PCR-Script/lePOCS using the EcoRI and the KpnI cleavage sites which flank the promoter at the 5' end and at the 3' end, respectively. Plasmid pBinAR-TkTp-9/sll0418 Δ SP was also treated with the restriction

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enzymes EcoRI and KpnI. As a consequence, the CaMV 35S promoter was excised from this plasmid. The promoter of the legumin gene was subsequently cloned into this vector as an EcoRI/KpnI fragment, thus generating a plasmid which placed the expression of the deletion clone of the *sll0418* gene under the control of this seed-specific promoter, see Figure 6. Fragment A (2700 bp) in Figure 6 contains the promoter of the *Vicia faba* legumin B4 gene, fragment B (245 bp) encodes the transit peptide of *Nicotiana tabacum* transketolase, fragment C (930 bp) encodes the *Synechocystis* spec. PCC6803 ORF *sll0418*ΔSP, and fragment D (219 bp) encodes the termination signal of the octopine synthase gene.

This plasmid (pBinARleP-TkTp-9/*sll0418*ΔSP) was used for the generation of transgenic *Arabidopsis thaliana*, *Brassica napus* and *Nicotiana tabacum* plants.

An increase in the tocopherol and tocotrienol contents was also measured by expressing the DNA sequence SEQ-ID No. 7 in transgenic plants.

Example 9

Generation of transgenic *Arabidopsis thaliana* plants

Wild-type *Arabidopsis thaliana* plants (Columbia) were transformed with the *Agrobacterium tumefaciens* strain (EHA105) using a modified vacuum infiltration method as the basis (Steve Clough and Andrew Bent. Floral dip: a simplified method for *Agrobacterium*-mediated transformation of *Arabidopsis thaliana*. Plant J 16(6):735-43, 1998; Bechtold, N., Ellis, J. and Pelltier, G., in: *Planta Agrobacterium-mediated gene transfer by infiltration of adult Arabidopsis thaliana plants*. CRAcad Sci Paris, 1993, 1144(2):204-212). The *Agrobacterium tumefaciens* cells used had previously been transformed with plasmids pBinAR-TkTp-9/*sll0418* or pBinARleP-TkTp-9/*sll0418* (Figure 3 and 4).

Seeds of the primary transformants were selected on the basis of antibiotic resistance. Antibiotic-resistant seedlings were planted into soil and used for biochemical analysis as fully developed plants.

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Example 10

Generation of transgenic Brassica napus plants

- 5 The generation of transgenic oilseed rape plants followed in principle a procedure described by Bade, J.B. and Damm, B. (in Gene Transfer to Plants, Potrykus, I. and Spangenberg, G., eds, Springer Lab Manual, Springer Verlag, 1995, 30-38), which also gives the composition of the media and buffers used.
- 10 The transformations were performed with *Agrobacterium tumefaciens* strain EHA105. Plasmids pBinAR-TkTp-9/sll0418 and pBinARleP-TkTp-9/sll0418 were used for the transformation. Seeds of Brassica napus var. Westar were surface-sterilized with 70% ethanol (v/v), washed in water for 10 minutes at 55°C, incubated for 20 minutes in 1% strength hypochlorite solution (25% v/v Teepol, 0.1% v/v Tween 20) and washed six times with sterile water for in each case 20 minutes. The seeds were dried on filter paper for three days, and 10-15 seeds were germinated in a glass
- 15 flask containing 15 ml of germination medium. The roots and apices were removed from several seedlings (approximate size 10 cm), and the hypocotyls which remained were cut into sections of approximate length 6 mm. The approximately 600 explants thus obtained were washed for 30 minutes with 50 ml of basal medium
- 20 and transferred into a 300 ml flask. After addition of 100 ml of callus induction medium, the cultures were incubated for 24 hours at 100 rpm.

- An overnight culture of the agrobacterial strain was established
- 30 in Luria broth medium supplemented with kanamycin (20 mg/l) at 29°C, and 2 ml of this were incubated in 50 ml of Luria broth medium without kanamycin for 4 hours at 29°C to an OD₆₀₀ of 0.4 - 0.5. After the culture had been pelleted for 25 minutes at 2000 rpm, the cell pellet was resuspended in 25 ml of basal
- 35 medium. The bacterial concentration in the solution was brought to an OD₆₀₀ of 0.3 by adding more basal medium.

- The callus induction medium was removed from the oilseed rape explants using sterile pipettes, 50 ml of agrobacterial
- 40 suspension were added, the cultures were mixed carefully and incubated for 20 minutes. The agrobacterial suspension was removed, the oilseed rape explants were washed for 1 minute with 50 ml of callus induction medium, and 100 ml of callus induction medium were subsequently added. Cocultivation was performed for
- 45 24 hours on an orbital shaker at 100 rpm. Cocultivation was stopped by removing the callus induction medium, and the explants were washed twice with 25 ml of wash medium for 1 minute each

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time and twice for 60 minutes with 100 ml of wash medium each time, at 100 rpm. The wash medium together with the explants was transferred into 15 cm Petri dishes, and the medium was removed using sterile pipettes.

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For regeneration, batches of 20-30 explants were transferred into 90 mm Petri dishes containing 25 ml of shoot induction medium supplemented with kanamycin. The Petri dishes were sealed with two layers of Leukopor and incubated at 25°C and 2000 lux at

- 10 photoperiods of 16 hours light/8 hours dark. Every 12 days, the developing calli were transferred to fresh Petri dishes containing shoot induction medium. All further steps for regenerating entire plants were carried out as described by Bade, J.B. and Damm, B. (in Gene Transfer to Plants, Potrykus, I. and Spangenberg, G., eds, Springer Lab Manual, Springer Verlag, 1995, 30-38).

Example 11

20 Generation of transgenic *Nicotiana tabacum* plants

10 ml of YEB medium supplemented with antibiotic (5 g/l beef extract, 1 g/l yeast extract, 5 g/l peptone, 5 g/l sucrose and 2 mM MgSO_4) were inoculated with a colony of *Agrobacterium*

- 25 *tumefaciens* and the culture was grown overnight at 28°C. The cells were pelleted for 20 minutes at 4°C, 3500 rpm, using a bench centrifuge and then resuspended under sterile conditions in fresh YEB medium without antibiotics. The cell suspension was used for the transformation.

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The sterile-grown wild-type plants were obtained by vegetative propagation. To this end, only the tip of the plant was cut off and transferred to fresh 2MS medium in a sterile preserving jar. As regards the rest of the plant, the hairs on the upper side of

- 35 the leaves were removed and the central veins of the leaves were removed. Using a razor blade, the leaves were cut into sections of approximate size 1 cm². The agrobacterial culture was transferred into a small Petri dish (diameter 2 cm). The leaf sections were briefly drawn through this solution and placed with
- 40 the underside of the leaves on 2MS medium in Petri dishes (diameter 9 cm) in such a way that they touched the medium. After two days in the dark at 25°C, the explants were transferred to plates with callus induction medium and warmed at 28°C in a controlled-environment cabinet. The medium had to be changed
- 45 every 7-10 days. As soon as calli formed, the explants were transferred into sterile preserving jars on shoot induction medium supplemented with claforan (see above). Organogenesis

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started after approximately one month and it was possible to cut off the shoots formed. The shoots were grown on 2MS medium supplemented with claforan and selection marker. As soon as a substantial root ball had developed, it was possible to pot up the plants in seed compost.

Example 12

Characterization of the transgenic plants

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To confirm that expression of the *Synechocystis* spec. PCC6803 2-methyl-6-phytylhydroquinone methyltransferase increased vitamin E biosynthesis in the transgenic plants, the tocopherol and tocotrienol contents in leaves and seeds of the plants

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transformed with the constructs pBinARleP-TkTp-9/sll0418 or pBinAR-TkTp-9/sll0418 (*Arabidopsis thaliana*, *Brassica napus* and *Nicotiana tabacum*) were analyzed. To this end, the transgenic plants were grown in the greenhouse, and plants which express the gene encoding the *Synechocystis* spec. PCC6803

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2-methyl-6-phytylhydroquinone methyltransferase were analyzed at Northern level. The tocopherol content and the tocotrienol content in leaves and seeds of these plants were determined. In all cases, the tocopherol or tocotrienol concentration in transgenic plants which additionally express a DNA sequence SEQ

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ID No. 1 or SEQ ID No. 7, was elevated in comparison with untransformed plants.

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We claim:

1. A DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence
5 hybridizing herewith or a DNA sequence which is homologous to
the full sequence or to subsequences, encoding a
Synechocystis 2-methyl-6-phytylhydroquinone
methyltransferase.
- 10 2. The use of DNA sequences encoding a
2-methyl-6-phytylhydroquinone methyltransferase for the
generation of plants and photosynthetically active organisms
with an elevated tocopherol and tocotrienol content.
- 15 3. The use of a DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a
DNA sequence hybridizing herewith encoding a
2-methyl-6-phytylhydroquinone methyltransferase for the
generation of plants and photosynthetically active organisms
with an elevated tocopherol and tocotrienol content.
- 20 4. A method for the generation of plants and photosynthetically
active organisms with an elevated tocopherol and tocotrienol
content, which comprises expressing, in plants and
photosynthetically active organisms, a DNA sequence SEQ ID
25 No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith
or a DNA sequence which is homologous to the full sequence or
to subsequences.
- 30 5. A method for the transformation of a plant, which comprises
introducing, into a plant cell, callus tissue, an entire
plant or protoplasts of plant cells, an expression cassette
containing a promoter, a signal sequence, a DNA sequence SEQ
ID No. 1 or SEQ ID No. 7 and a terminator or a DNA sequence
35 hybridizing with this expression cassette.
- 40 6. The method for the transformation of plants as claimed in
claim 5, wherein transformation is done with the aid of the
strain *Agrobacterium tumefaciens*, electroporation or the
particle bombardment method.
7. A plant with an elevated tocopherol and tocotrienol content
comprising an expression cassette as claimed in claim 5.
- 45 drawings

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8. A plant as claimed in claim 7 selected from the group consisting of soya, canola, barley, oats, wheat, oilseed rape, corn, rye, tagetes or sunflower.
- 5 9. The use of a DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith as claimed in claim 1 for the preparation of a test system for identifying 2-methyl-6-phytylhydroquinone methyltransferase inhibitors.
- 10 10. A test system based on the expression of a DNA sequence SEQ ID No. 1 or SEQ ID No. 7 or a DNA sequence hybridizing herewith as claimed in claim 1 for identifying 2-methyl-6-phytylhydroquinone methyltransferase inhibitors.

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Identification and overexpression of a DNA sequence encoding a
2-methyl-6-phytylhydroquinone methyltransferase in plants

5 Abstract

Process for the generation of plants with an elevated tocopherol
and tocotrienol content by overexpressing a gene encoding a
2-methyl-6-phytylhydroquinone methyltransferase.

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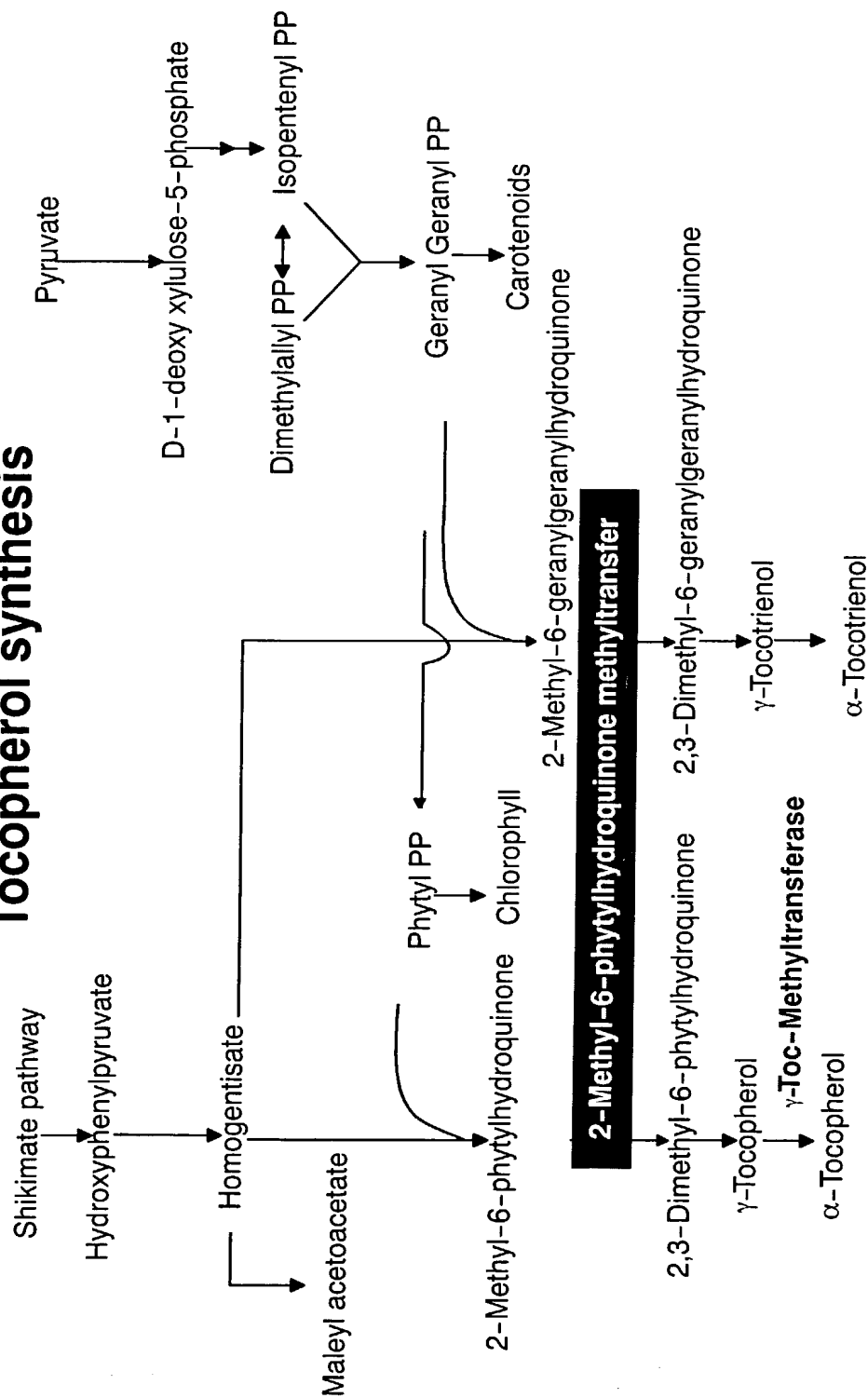
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Figure 1

Tocopherol synthesis



0817/00001

Figure 2

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Figure 3

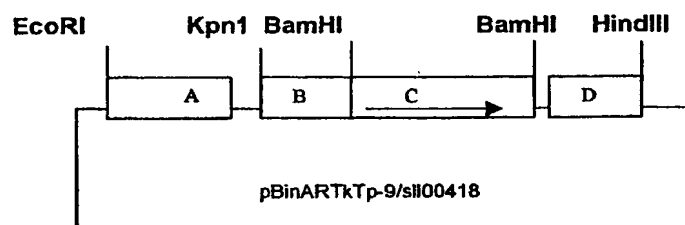


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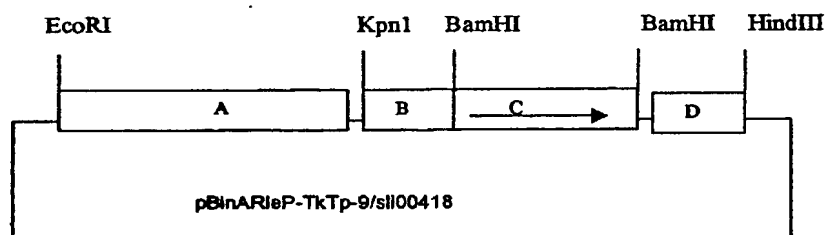


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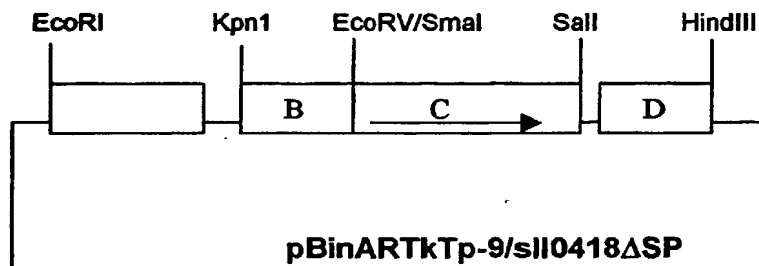
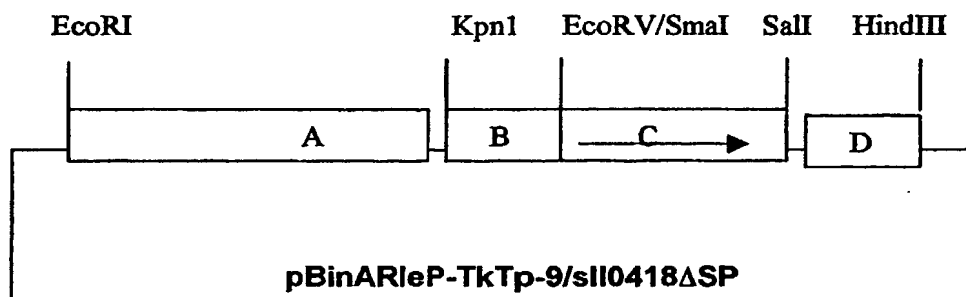


Figure 6



Declaration, Power of Attorney and Petition

Page 1 of 3

0817/000001

We (I), the undersigned inventor(s), hereby declare(s) that:

My residence, post office address and citizenship are as stated below next to my name,

We (I) believe that we are (I am) the original, first, and joint (sole) inventor(s) of the subject matter which is claimed and for which a patent is sought on the invention entitled

IDENTIFICATION AND OVEREXPRESSION OF A DNA SEQUENCE
ENCODING A 2-METHYL-6-PHYTYLHYDROQUINONE
METHYLTRANSFERASE IN PLANTS ✓

the specification of which

☒ is attached hereto.

☐ was filed on _____ as

Application Serial No. _____

and amended on _____.

☒ was filed as PCT international application

Number PCT/EP/00/05862 ✓

on 23 June 2000 ✓

and was amended under PCT Article 19

on _____ (if applicable).

We (I) hereby state that we (I) have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

We (I) acknowledge the duty to disclose information known to be material to the patentability of this application as defined in Section 1.56 of Title 37 Code of Federal Regulations.

We (I) hereby claim foreign priority benefits under 35 U.S.C. § 119(a)–(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed. Prior Foreign Application(s)

Application No.	Country	Day/Month/Year	Priority Claimed
19931834.4 ✓	Germany ✓	09 July 1999 ✓	<input checked="" type="checkbox"/> Yes <input type="checkbox"/> No

0817/000001

We (I) hereby claim the benefit under Title 35, United States Codes, § 119(e) of any United States provisional application(s) listed below.

_____ (Application Number)	_____ (Filing Date)
_____ (Application Number)	_____ (Filing Date)

We (I) hereby claim the benefit under 35 U.S.C. § 120 of any United States application(s), or § 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. § 112, I acknowledge the duty to disclose information which is material to patentability as defined in 37 CFR § 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application.

Application Serial No.	Filing Date	Status (pending, patented, abandoned)
_____	_____	_____
_____	_____	_____
_____	_____	_____

2 - And we (I) hereby appoint **HERBERT. B. KEIL**, Registration Number 18,967; and **RUSSEL E. WEINKAUF**, Registration Number 18,495; the address of both being Messrs. Keil & Weinkauff, 1101 Connecticut Ave., N.W., Washington, D.C. 20036 (telephone 202-659-0100), our attorneys, with full power of substitution and revocation, to prosecute this application, to make alterations and amendments therein, to sign the drawings, to receive the patent, and to transact all business in the Patent Office connected therewith.

We (I) declare that all statements made herein of our (my) own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

0817/000001

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SEQUENCE LISTING

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Ser Leu Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr	
15 20 25 30	
cag tca tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac	144
Gln Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp	
35 40 45	
ggc att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat	192
Gly Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr	
50 55 60	
ggc gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt	240
Gly Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe	
65 70 75	
gtc cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc	288
Val His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly	
80 85 90	
aca acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att	336
Thr Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile	
95 100 105 110	
ctc gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc	384
Leu Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro	
115 120 125	
caa cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc	432
Gln Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala	
130 135 140	
aag ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt	480
Lys Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser	
145 150 155	
ttc gac gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa	528
Phe Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys	
160 165 170	
gct gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att	576

Ala Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile
 175 180 185 190

ctg gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc 624
 Leu Val Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu
 195 200 205

aac ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc 672
 Asn Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser
 210 215 220

cac cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc 720
 His Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala
 225 230 235

acg ggt ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg 768
 Thr Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro
 240 245 250

acc ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc 816
 Thr Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro
 255 260 265 270

cag ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg 864
 Gln Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg
 275 280 285

gaa gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt 912
 Glu Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu
 290 295 300

tgt cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct 960
 Cys Arg Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
 305 310 315

taa attgcggatc c 974

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 <212> PRT
 <213> Synechocystis PCC6803

<400> 4

Met Pro Glu Tyr Leu Leu Leu Pro Ala Gly Leu Ile Ser Leu Ser Leu
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Ala Ile Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser
 20 25 30

Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile
 35 40 45

Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp
 50 55 60

Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His
 65 70 75 80

Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr
85 90 95

Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala
100 105 110

Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln
115 120 125

Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe
130 135 140

Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp
145 150 155 160

Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val
165 170 175

Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val
180 185 190

Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe
195 200 205

Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro
210 215 220

Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly
225 230 235 240

Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu
245 250 255

Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly
260 265 270

Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val
275 280 285

Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg
290 295 300

Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
305 310 315

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<211> 27
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<213> Synechocystis PCC6803

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<400> 5

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7

<210> 6
<211> 26
<212> DNA
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<220>
<221> primer_bind
<222> (1)..(26)

<400> 6

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<222> (10)..(915)

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Met Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln
1 5 10

tca tcg gat tcc gtg gcc aac gcc tac gac caa tgg aca gag gac ggc 99
Ser Ser Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly
15 20 25 30

att ttg gaa tat tac tgg ggc gac cat atc cac ctc ggc cat tat ggc 147
Ile Leu Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly
35 40 45

gat ccg cca gtg gcc aag gat ttc atc caa tcg aaa att gat ttt gtc 195
Asp Pro Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val
50 55 60

cat gcc atg gcc cag tgg ggc gga tta gat aca ctt ccc ccc ggc aca 243
His Ala Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr
65 70 75

acg gta ttg gat gtg ggt tgc ggc att ggc ggt agc agt cgc att ctc 291
Thr Val Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu
80 85 90

gcc aaa gat tat ggt ttt aac gtt acc ggc atc acc att agt ccc caa 339
Ala Lys Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln
95 100 105 110

cag gtg aaa cgg gcg acg gaa tta act cct ccc gat gtg acg gcc aag 387
Gln Val Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys
115 120 125

8

ttt gcg gtg gac gat gct atg gct ttg tct ttt cct gac ggt agt ttc 435
 Phe Ala Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe
 130 135 140

gac gta gtt tgg tcg gtg gaa gca ggg ccc cac atg cct gac aaa gct 483
 Asp Val Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala
 145 150 155

gtg ttt gcc aag gaa tta ctg cgg gtc gtg aaa cca ggg ggc att ctg 531
 Val Phe Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu
 160 165 170

gtg gtg gcg gat tgg aat caa cgg gac gat cgc caa gtg ccc ctc aac 579
 Val Val Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn
 175 180 185 190

ttc tgg gaa aaa cca gtg atg cga caa ctg ttg gat caa tgg tcc cac 627
 Phe Trp Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His
 195 200 205

cct gcc ttt gcc agc att gaa ggt ttt gcg gaa aat ttg gaa gcc acg 675
 Pro Ala Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr
 210 215 220

ggt ttg gtg gag ggc cag gtg act act gct gat tgg act gta ccg acc 723
 Gly Leu Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr
 225 230 235

ctc ccc gct tgg ttg gat acc att tgg cag ggc att atc cgg ccc cag 771
 Leu Pro Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln
 240 245 250

ggc tgg tta caa tac ggc att cgt ggg ttt atc aaa tcc gtg cgg gaa 819
 Gly Trp Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu
 255 260 265 270

gta ccg act att tta ttg atg cgc ctt gcc ttt ggg gta gga ctt tgt 867
 Val Pro Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys
 275 280 285

cgc ttc ggt atg ttc aaa gca gtg cga aaa aac gcc act caa gct taa 915
 Arg Phe Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
 290 295 300

attcttaagg tcgac 930

<210> 8

<211> 301

<212> PRT

<213> Synechocystis PCC6803

<400> 8

Met Ala Ala Gly Leu Tyr Leu Leu Thr Ala Arg Gly Tyr Gln Ser Ser
 1 5 10 15

Asp Ser Val Ala Asn Ala Tyr Asp Gln Trp Thr Glu Asp Gly Ile Leu
 20 25 30

Glu Tyr Tyr Trp Gly Asp His Ile His Leu Gly His Tyr Gly Asp Pro
 35 40 45
 Pro Val Ala Lys Asp Phe Ile Gln Ser Lys Ile Asp Phe Val His Ala
 50 55 60
 Met Ala Gln Trp Gly Gly Leu Asp Thr Leu Pro Pro Gly Thr Thr Val
 65 70 75 80
 Leu Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Ile Leu Ala Lys
 85 90 95
 Asp Tyr Gly Phe Asn Val Thr Gly Ile Thr Ile Ser Pro Gln Gln Val
 100 105 110
 Lys Arg Ala Thr Glu Leu Thr Pro Pro Asp Val Thr Ala Lys Phe Ala
 115 120 125
 Val Asp Asp Ala Met Ala Leu Ser Phe Pro Asp Gly Ser Phe Asp Val
 130 135 140
 Val Trp Ser Val Glu Ala Gly Pro His Met Pro Asp Lys Ala Val Phe
 145 150 155 160
 Ala Lys Glu Leu Leu Arg Val Val Lys Pro Gly Gly Ile Leu Val Val
 165 170 175
 Ala Asp Trp Asn Gln Arg Asp Asp Arg Gln Val Pro Leu Asn Phe Trp
 180 185 190
 Glu Lys Pro Val Met Arg Gln Leu Leu Asp Gln Trp Ser His Pro Ala
 195 200 205
 Phe Ala Ser Ile Glu Gly Phe Ala Glu Asn Leu Glu Ala Thr Gly Leu
 210 215 220
 Val Glu Gly Gln Val Thr Thr Ala Asp Trp Thr Val Pro Thr Leu Pro
 225 230 235 240
 Ala Trp Leu Asp Thr Ile Trp Gln Gly Ile Ile Arg Pro Gln Gly Trp
 245 250 255
 Leu Gln Tyr Gly Ile Arg Gly Phe Ile Lys Ser Val Arg Glu Val Pro
 260 265 270
 Thr Ile Leu Leu Met Arg Leu Ala Phe Gly Val Gly Leu Cys Arg Phe
 275 280 285
 Gly Met Phe Lys Ala Val Arg Lys Asn Ala Thr Gln Ala
 290 295 300

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<400> 10

gtcgacctta agaatttaag cttgagtggc g

31